

RAW SEQUENCE LISTING

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Application Serial Number: 10/048,116B
Source: IFW16
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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/048,116B

DATE: 04/20/2006

TIME: 09:51:03

Input Set : A:\seq list.txt
 Output Set: N:\CRF4\04202006\J048116B.raw

3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6 FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7 IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
 11 <140> CURRENT APPLICATION NUMBER: 10/048,116B
 12 <141> CURRENT FILING DATE: 2002-02-27
 14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
 15 <151> PRIOR FILING DATE: 2000-07-28
 17 <150> PRIOR APPLICATION NUMBER: FR99/09862
 18 <151> PRIOR FILING DATE: 1999-07-29
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1517
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
 31 coding IAalpha(d)/Fc
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (18)..(1502)
 37 <400> SEQUENCE: 1
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 39 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
 40 1 5 10
 42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att 98
 43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
 44 15 20 25
 46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct 146
 47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
 48 30 35 40
 50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc 194
 51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
 52 45 50 55
 54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt 242
 55 Tyr Val Asp Leu Asp Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
 56 60 65 70 75
 58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct 290
 59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
 60 80 85 90
 62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc 338

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63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr			
64 95	100	105	
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct	386		
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro			
68 110	115	120	
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc	434		
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile			
72 125	130	135	
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc	482		
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val			
76 140	145	150	155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc	530		
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser			
80 160	165	170	
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att	578		
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile			
84 175	180	185	
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa	626		
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys			
88 190	195	200	
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act	674		
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr			
92 205	210	215	
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag	722		
95 Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu			
96 220	225	230	235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttgcaa	770		
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln			
100 240	245	250	
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc	818		
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro			
104 255	260	265	
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg	866		
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu			
108 270	275	280	
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc	914		
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu			
112 285	290	295	
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gat gtg agc	962		
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser			
116 300	305	310	315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa	1010		
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu			
120 320	325	330	
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act	1058		
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr			
124 335	340	345	
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt	1106		
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser			

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128	350	355	360	
130	ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc			1154
131	Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro			
132	365	370	375	
134	atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag			1202
135	Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln			
136	380	385	390	395
138	gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc			1250
139	Val Tyr Val Leu Pro Pro Glu Glu Met Thr Lys Lys Gln Val			
140	400	405	410	
142	act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg			1298
143	Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val			
144	415	420	425	
146	gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa			1346
147	Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu			
148	430	435	440	
150	cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga			1394
151	Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg			
152	445	450	455	
154	gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg			1442
155	Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val			
156	460	465	470	475
158	gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg			1490
159	Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg			
160	480	485	490	
162	act ccg ggt aaa tgatgactcg acctg			1517
163	Thr Pro Gly Lys			
164	495			
167	<210> SEQ ID NO: 2			
168	<211> LENGTH: 495			
169	<212> TYPE: PRT			
170	<213> ORGANISM: Artificial Sequence			
172	<220> FEATURE:			
173	<223> OTHER INFORMATION: Description of Artificial Sequence: construct			
174	coding IAalpha(d)/Fc			
176	<400> SEQUENCE: 2			
177	Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr			
178	1	5	10	15
180	Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val			
181	20	25	30	
183	Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln			
184	35	40	45	
186	Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp			
187	50	55	60	
189	Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu			
190	65	70	75	80
192	Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn			
193	85	90	95	
195	Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu			

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196	100	105	110
198	Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln		
199	115	120	125
201	Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile		
202	130	135	140
204	Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr		
205	145	150	155
207	Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser		
208	165	170	175
210	Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val		
211	180	185	190
213	Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu		
214	195	200	205
216	Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Ser		
217	210	215	220
219	Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu		
220	225	230	235
222	Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu		
223	245	250	255
225	Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys		
226	260	265	270
228	Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val		
229	275	280	285
231	Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser		
232	290	295	300
234	Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp		
235	305	310	315
237	Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln		
238	325	330	335
240	Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser		
241	340	345	350
243	Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys		
244	355	360	365
246	Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile		
247	370	375	380
249	Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro		
250	385	390	395
252	Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met		
253	405	410	415
255	Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn		
256	420	425	430
258	Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser		
259	435	440	445
261	Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn		
262	450	455	460
264	Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu		
265	465	470	475
267	His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys		
268	485	490	495

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271 <210> SEQ ID NO: 3
272 <211> LENGTH: 1485
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence:coding region
278      of SEQ ID NO:1
280 <220> FEATURE:
281 <221> NAME/KEY: CDS
282 <222> LOCATION: (1)..(1485)
284 <400> SEQUENCE: 3
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286 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
287      1           5           10          15
289 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta    96
290 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
291      20          25          30
293 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag    144
294 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
295      35          40          45
297 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat    192
298 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
299      50          55          60
301 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc    240
302 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
303      65          70          75          80
305 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac    288
306 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
307      85          90          95
309 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag    336
310 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
311      100         105         110
313 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag    384
314 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
315      115         120         125
317 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc    432
318 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
319      130         135         140
321 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat    480
322 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
323      145         150         155         160
325 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct    528
326 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
327      165         170         175
329 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg    576
330 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val
331      180         185         190
333 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag    624
334 Glu His Trp Gly Leu Glu Pro Val Leu Lys His Trp Glu Pro Glu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/048,116B

DATE: 04/20/2006

TIME: 09:51:04

Input Set : A:\seq list.txt

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